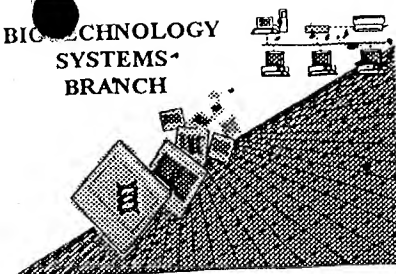


## RAW SEQUENCE LISTING ERROR REPORT

BIO-TECHNOLOGY  
SYSTEMS-  
BRANCH



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/808504  
Source: O I P E  
Date Processed by STIC: 10/04/01

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER  
VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND  
TRADEMARK OFFICE WEBSITE. SEE BELOW:

### Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:  
<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 09/808504
ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO		
1 <input type="checkbox"/> Wrapped Nucleics Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."	
2 <input type="checkbox"/> Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.	
3 <input type="checkbox"/> Misaligned Amino Numbering	The numbering under each 5 <sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.	
4 <input type="checkbox"/> Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.	
5 <input type="checkbox"/> Variable Length	Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.	
6 <input type="checkbox"/> PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.	
7 <input type="checkbox"/> Skipped Sequences (OLD RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped  Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.	
8 <input type="checkbox"/> Skipped Sequences (NEW RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence: <210> sequence id number <400> sequence id number 000	
9 <input type="checkbox"/> Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.	
10 <input type="checkbox"/> Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence	
11 <input type="checkbox"/> Use of <220>	Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)	
12 <input type="checkbox"/> PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	
13 <input checked="" type="checkbox"/> Misuse of n	n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.	

OIPE

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/808,504

DATE: 10/04/2001

TIME: 17:52:30

Input Set : A:\9693004999.txt

Output Set: N:\CRF3\10042001\I808504.raw

Does Not Comply  
Corrected Diskette Needed

4 <110> APPLICANT: Platica, Ovidiu  
 6 <120> TITLE OF INVENTION: METHOD OF SIMULTANEOUS DETECTION OF BASE CHANGES (SDBC) IN  
 EXPRESSED

7 GENES

9 &lt;130&gt; FILE REFERENCE: 9693-004

11 &lt;140&gt; CURRENT APPLICATION NUMBER: 09/808,504

C--&gt; 12 &lt;141&gt; CURRENT FILING DATE: 2001-09-21

14 &lt;160&gt; NUMBER OF SEQ ID NOS: 12

16 &lt;170&gt; SOFTWARE: PatentIn version 3.1

18 &lt;210&gt; SEQ ID NO: 1

19 &lt;211&gt; LENGTH: 19

20 &lt;212&gt; TYPE: DNA

C--&gt; 21 &lt;213&gt; ORGANISM: Artificial FYI: "Artificial Sequence" is the preferred nomenclature

23 &lt;220&gt; FEATURE:

24 &lt;223&gt; OTHER INFORMATION: Description of Artificial Sequence: Primer

26 &lt;400&gt; SEQUENCE: 1

27 ctatagtgtc acctaaata

19

29 &lt;210&gt; SEQ ID NO: 2

30 &lt;211&gt; LENGTH: 70

31 &lt;212&gt; TYPE: DNA

C--&gt; 32 &lt;213&gt; ORGANISM: Artificial

34 &lt;220&gt; FEATURE:

35 &lt;223&gt; OTHER INFORMATION: Description of Artificial Sequence: Example of 'Stuffer'

Sequence as

36 described in the Specification

38 &lt;400&gt; SEQUENCE: 2

39 gggtttttcta tagtgtcacc taaataacgc gtcgacgtcg cgatcccttt agtgagggtt

60

40 aatgggtttt

70

42 &lt;210&gt; SEQ ID NO: 3

43 &lt;211&gt; LENGTH: 70

44 &lt;212&gt; TYPE: DNA

C--&gt; 45 &lt;213&gt; ORGANISM: Artificial

47 &lt;220&gt; FEATURE:

48 &lt;223&gt; OTHER INFORMATION: Description of Artificial Sequence: Example of 'Stuffer'

Sequence as

49 described in the Specification

51 &lt;400&gt; SEQUENCE: 3

52 aaaacccatt aaccctcact aaagggtatcg cgacgtcgac gcgttattta ggtgacacta

60

53 tagaaaaccc

70

55 &lt;210&gt; SEQ ID NO: 4

56 &lt;211&gt; LENGTH: 20

57 &lt;212&gt; TYPE: DNA

C--&gt; 58 &lt;213&gt; ORGANISM: Artificial

60 &lt;220&gt; FEATURE:

61 &lt;223&gt; OTHER INFORMATION: Description of Artificial Sequence: Primer

63 &lt;400&gt; SEQUENCE: 4

64 attaacctc actaaaggga

20

66 &lt;210&gt; SEQ ID NO: 5

\*67 <211> LENGTH: 38  
68 <212> TYPE: DNA

## RAW SEQUENCE LISTING

DATE: 10/04/2001

PATENT APPLICATION: US/09/808,504

TIME: 17:52:30

Input Set : A:\9693004999.txt

Output Set: N:\CRF3\10042001\I808504.raw

```

C--> 69 <213> ORGANISM: Artificial
      71 <220> FEATURE:
      72 <223> OTHER INFORMATION: Description of Artificial Sequence: 'Stuffer' with ligating
ends
      74 <220> FEATURE:
      75 <221> NAME/KEY: misc_feature
      76 <222> LOCATION: (18)..(18) Erased
      77 <223> OTHER INFORMATION: n = a 'stuffer' sequence as described in the Specification
      79 <400> SEQUENCE: 5 n may only represent a single nucleotide base.
W--> 80 atgtgtgggg ttttctanaa tgggttttga ttgaagct 38
      82 <210> SEQ ID NO: 6
      83 <211> LENGTH: 6
      84 <212> TYPE: PRT
      85 <213> ORGANISM: Homo sapiens
      87 <220> FEATURE:
      88 <221> NAME/KEY: misc_feature
      89 <222> LOCATION: (3)..(3)
      90 <223> OTHER INFORMATION: Xaa = Glu, Val, Gly, or Ala
      92 <400> SEQUENCE: 6
W--> 93 Ile Cys Xaa Ile Glu Ala
      94 1 5
      96 <210> SEQ ID NO: 7
      97 <211> LENGTH: 18
      98 <212> TYPE: DNA
      99 <213> ORGANISM: Homo sapiens
     101 <220> FEATURE:
     102 <221> NAME/KEY: misc_feature
     103 <222> LOCATION: (8)..(8)
     104 <223> OTHER INFORMATION: n = a, t, c, or g
     106 <400> SEQUENCE: 7
W--> 107 atgtgtgnga ttgaagct 18
     109 <210> SEQ ID NO: 8
     110 <211> LENGTH: 6
     111 <212> TYPE: PRT
     112 <213> ORGANISM: Homo sapiens
     114 <400> SEQUENCE: 8
     115 Ile Cys Val Ile Glu Ala
     116 1 5
     118 <210> SEQ ID NO: 9
     119 <211> LENGTH: 18
     120 <212> TYPE: DNA
     121 <213> ORGANISM: Homo sapiens
     123 <400> SEQUENCE: 9
     124 atgtgtgtga ttgaagct 18
     126 <210> SEQ ID NO: 10
     127 <211> LENGTH: 6
     128 <212> TYPE: PRT
     129 <213> ORGANISM: Homo sapiens
     131 <400> SEQUENCE: 10
     132 Ile Cys Glu Ile Glu Ala

```

## RAW SEQUENCE LISTING

DATE: 10/04/2001

PATENT APPLICATION: US/09/808,504

TIME: 17:52:30

Input Set : A:\9693004999.txt

Output Set: N:\CRF3\10042001\I808504.raw

```
133 1          5
135 <210> SEQ ID NO: 11
136 <211> LENGTH: 18
137 <212> TYPE: DNA
138 <213> ORGANISM: Homo sapiens
140 <400> SEQUENCE: 11
141 atgtgtgaga ttgaagct                                18
143 <210> SEQ ID NO: 12
144 <211> LENGTH: 19
145 <212> TYPE: DNA
C--> 146 <213> ORGANISM: Artificial
148 <220> FEATURE:
149 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
151 <400> SEQUENCE: 12
152 tatttaggtg tcactatag                                19
```

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/808,504

DATE: 10/04/2001

TIME: 17:52:31

Input Set : A:\9693004999.txt

Output Set: N:\CRF3\10042001\I808504.raw

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:21 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:1  
L:32 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:2  
L:45 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:3  
L:58 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:4  
L:69 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:5  
L:80 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5  
L:93 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6  
L:107 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7  
L:146 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:12